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#31

RAW SEQUENCE LISTING

DATE: 04/18/2003

PATENT APPLICATION: US/09/267,963D

TIME: 14:22:06

Input Set : N:\Crf4\04072003\I267963B.raw

Output Set: N:\CRF4\04182003\I267963D.raw

1 <110> APPLICANT: MIYAZONO, Kohei
 2 IMAMURA, Takeshe
 3 DEN DIJKE, Peter
 4 <120> TITLE OF INVENTION: PROTEINS HAVING SERINE/THREONINE KINASE DOMAINS,
 CORRESPONDING

5 NUCLEIC ACID MOLECULES AND THEIR USE
 6 <130> FILE REFERENCE: LUD 5539.1 CIP
 C--> 7 <140> CURRENT APPLICATION NUMBER: US/09/267,963D
 8 <141> CURRENT FILING DATE: 1999-03-12
 9 <150> PRIOR APPLICATION NUMBER: PCT/GB93/02367
 10 <151> PRIOR FILING DATE: 1993-11-17
 11 <150> PRIOR APPLICATION NUMBER: US 09/039,177
 12 <151> PRIOR FILING DATE: 1998-03-13
 13 <160> NUMBER OF SEQ ID NOS: 46
 14 <170> SOFTWARE: PatentIn version 3.2
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1984
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 20 <400> SEQUENCE: 1

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23	gagcgagccc	ctccccggt	ccagcccggg	ccggggccgc	gccggacccc	agcccgccgt	180
24	ccagcgctgg	cggtgcaact	gcggccgcgc	ggtggagggg	aggtggcccc	ggtccgccga	240
25	aggctagcgc	cccgccaccc	gcagagcggg	cccagaggga	ccatgacctt	gggtccccc	300
26	aggaaaggcc	ttctgatgct	gctgatggcc	ttggtgacct	agggagacct	tgtgaagccg	360
27	tctcggggcc	cgctggtgac	ctgcacgtgt	gagagcccac	attgcaaggg	gcctacctgc	420
28	cggggggcct	ggtgcacagt	agtgtgtgtg	cgggaggagg	ggaggcaccc	ccaggaacat	480
29	cggggctgcg	ggaacttgca	cagggagctc	tgcagggggc	gccccaccga	gttcgtcaac	540
30	cactactgct	gcgacagcca	cctctgcaac	cacaacgtgt	ccctggtgct	ggaggccacc	600
31	caacctcctt	cggagcagcc	gggaacagat	ggccagctgg	ccctgatcct	gggccccgtg	660
32	ctggccttgc	tggccctggt	ggccctgggt	gtcctggggc	tgtggcatgt	ccgacggagg	720
33	caggagaagc	agcgtggcct	gcacagcgag	ctgggagagt	ccagtctcat	cctgaaagca	780
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37	gccgtcaaga	tcttctctct	gagggatgaa	cagtcttggt	tccgggagac	tgagatctat	1020
38	aacacagtat	tgctcagaca	cgacaacatc	ctaggcttca	tcgcctcaga	catgacctcc	1080
39	cgcaactcga	gcacgcagct	gtggctcatc	acgcactacc	acgagcacgg	ctccctctac	1140
40	gactttctgc	agagacagac	gctggagccc	catctggctc	tgaggctagc	tgtgtcccg	1200
41	gcattgcggc	tggcgcaact	gcacgtggag	atcttcggta	cacagggcaa	accagccatt	1260
42	gccaccgcg	acttcaagag	ccgcaatgtg	ctgggtcaaga	gcaacctgca	gtgttgcatc	1320
43	gccgacctgg	gcctggctgt	gatgcactca	cagggcagcg	attacctgga	catcggaac	1380
44	aaccgcagag	tgggcaccaa	gcggtacatg	gcacccgagg	tgctggacga	gcagatccgc	1440

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46  gagattgccc gccggaccat cgtgaatggc atcgtggagg actatagacc acccttctat 1560
47  gatgtggtgc ccaatgaccc cagctttgag gacatgaaga aggtgggtgtg tgtggatcag 1620
48  cagaccccca ccatccctaa ccggttggt gcagaccgg tcctctcagg cctagctcag 1680
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50  aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800
51  agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatggtgcc 1860
52  ctatctgggt agaggtagt tgagtgtggt gtgtgctggg gatgggcagc tgcgcctgcc 1920
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65  Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
66  35 40 45
67  Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
68  50 55 60
69  Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
70  65 70 75 80
71  Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
72  85 90 95
73  His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
74  100 105 110
75  Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
76  115 120 125
77  Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
78  130 135 140
79  Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
80  145 150 155 160
81  Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
82  165 170 175
83  Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
84  180 185 190
85  Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
86  195 200 205
87  Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
88  210 215 220
89  Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
90  225 230 235 240
91  Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile
92  245 250 255
93  Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
94  260 265 270

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96          275                      280                      285
97      Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
98          290                      295                      300
99      Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
100         305                      310                      315                      320
101      Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
102          325                      330                      335
103      Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
104          340                      345                      350
105      Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
106          355                      360                      365
107      Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
108          370                      375                      380
109      Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
110         385                      390                      395                      400
111      Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
112          405                      410                      415
113      Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
114          420                      425                      430
115      Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
116          435                      440                      445
117      Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
118          450                      455                      460
119      Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
120         465                      470                      475                      480
121      Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
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123      Glu Lys Pro Lys Val Ile Gln
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130 <400> SEQUENCE: 3
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133      gattcttccg gtgcttatca tgattgctct cccctccctc agtatggaag atgagaagcc      180
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136      ccagaaaggc tgcttccagg tttatgagca gggaaagatg acctgtaaga ccccgccgtc      360
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138      gctgcccact aaaggaaaat ccttccctgg aacacagaat ttccacttgg aggttggcct      480
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140      ccgaaaattt aaaaggcgca accaagaacg cctcaatccc cgagacgtgg agtatggcac      600
141      tatcgaaggg ctcatcacca ccaatgttgg agacagcact ttagcagatt tattggatca      660
142      ttctgtgtaca tcaggaagtg gctctggtct tccttttctg gtacaaagaa cagtggctcg      720
143      ccagattaca ctgttggagt gtgtcgggaa aggcaggtat ggtgaggtgt ggaggggcag      780
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Output Set: N:\CRF4\04182003\I267963D.raw

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147 tgaaatgga tcgttgtacg actatcttca gcttactact ctggatacag ttagctgcct 1020
148 tcgaatagtg ctgtccatag ctagtgggtc tgcacatttg cacatagaga tatttgggac 1080
149 ccaagggaaa ccagccattg cccatcgaga tttaaagagc aaaaatattc tggtaagaa 1140
150 gaatggacag tgttgcatag cagatttggg cctggcagtc atgcattccc agagcaccaa 1200
151 tcagcttgat gtggggaaca atccccgtgt gggcaccaag cgctacatgg cccccgaagt 1260
152 tctagatgaa accatccagg tggattgttt cgattcttat aaaagggtcg atatttgggc 1320
153 ctttgacctt gttttgtggg aagtggccag gcggtggtg agcaatggtg tagtggagga 1380
154 ttacaagcca ccgttctacg atgtggttcc caatgaccca agttttgaag atatgaggaa 1440
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168 ctgatgttta caatgatgcc gaacattagg aattgtttat acacaacttt gcaaattatt 2280
169 tattacttgt gcacttagta gtttttacia aactgctttg tgcataatgt aaagcttatt 2340
170 tttatgtggt cttatgattt tattacagaa atgtttttaa cactatactc taaaatggac 2400
171 attttctttt attatcagtt aaaatcacat ttttaagtgt tcacatttgt atgtgtgtag 2460
172 actgtaactt tttttcagtt catatgcaga acgtatttag ccattaccca cgtgacacca 2520
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174 ggggaaaatg cattttcttc agaattatcc attacgtgca tttaaactct gccagaaaaa 2640
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178 <210> SEQ ID NO: 4

179 <211> LENGTH: 509

180 <212> TYPE: PRT

181 <213> ORGANISM: Homo sapiens

182 <400> SEQUENCE: 4

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186 20 25 30
187 Tyr Met Cys Val Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys
188 35 40 45
189 Glu Gly Gln Gln Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His
190 50 55 60
191 Val Tyr Gln Lys Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr
192 65 70 75 80
193 Cys Lys Thr Pro Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly
194 85 90 95

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200               130               135               140
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202   145               150               155               160
203   Asp Val Glu Tyr Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly
204               165               170               175
205   Asp Ser Thr Leu Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser
206               180               185               190
207   Gly Ser Gly Leu Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile
208               195               200               205
209   Thr Leu Leu Glu Cys Val Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg
210               210               215               220
211   Gly Ser Trp Gln Gly Glu Asn Val Ala Val Lys Ile Phe Ser Ser Arg
212   225               230               235               240
213   Asp Glu Lys Ser Trp Phe Arg Glu Thr Glu Leu Tyr Asn Thr Val Met
214               245               250               255
215   Leu Arg His Glu Asn Ile Leu Gly Phe Ile Ala Ser Asp Met Thr Ser
216               260               265               270
217   Arg His Ser Ser Thr Gln Leu Trp Leu Ile Thr His Tyr His Glu Met
218               275               280               285
219   Gly Ser Leu Tyr Asp Tyr Leu Gln Leu Thr Thr Leu Asp Thr Val Ser
220               290               295               300
221   Cys Leu Arg Ile Val Leu Ser Ile Ala Ser Gly Leu Ala His Leu His
222   305               310               315               320
223   Ile Glu Ile Phe Gly Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp
224               325               330               335
225   Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn Gly Gln Cys Cys Ile
226               340               345               350
227   Ala Asp Leu Gly Leu Ala Val Met His Ser Gln Ser Thr Asn Gln Leu
228               355               360               365
229   Asp Val Gly Asn Asn Pro Arg Val Gly Thr Lys Arg Tyr Met Ala Pro
230               370               375               380
231   Glu Val Leu Asp Glu Thr Ile Gln Val Asp Cys Phe Asp Ser Tyr Lys
232   385               390               395               400
233   Arg Val Asp Ile Trp Ala Phe Gly Leu Val Leu Trp Glu Val Ala Arg
234               405               410               415
235   Arg Met Val Ser Asn Gly Ile Val Glu Asp Tyr Lys Pro Pro Phe Tyr
236               420               425               430
237   Asp Val Val Pro Asn Asp Pro Ser Phe Glu Asp Met Arg Lys Val Val
238               435               440               445
239   Cys Val Asp Gln Gln Arg Pro Asn Ile Pro Asn Arg Trp Phe Ser Asp
240               450               455               460
241   Pro Thr Leu Thr Ser Leu Ala Lys Leu Met Lys Glu Cys Trp Tyr Gln
242   465               470               475               480
243   Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg Ile Lys Lys Thr Leu Thr

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/267,963D

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Input Set : N:\Crf4\04072003\I267963B.raw
Output Set: N:\CRF4\04182003\I267963D.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:19; N Pos. 20
Seq#:26; Xaa Pos. 2,4,5
Seq#:43; Xaa Pos. 2,3,4,5,6
Seq#:44; Xaa Pos. 1,3,4,6

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 4

VERIFICATION SUMMARY

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Input Set : N:\Crf4\04072003\I267963B.raw

Output Set: N:\CRF4\04182003\I267963D.raw

L:7 M:270 C: Current Application Number differs, Wrong Format
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:1134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:1591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:1617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0